

Supplementary Information

Robust direct digital-to-biological data storage in living cells

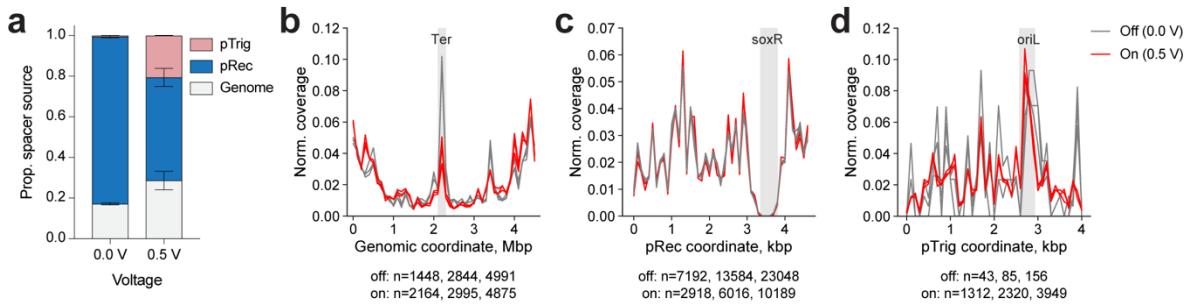
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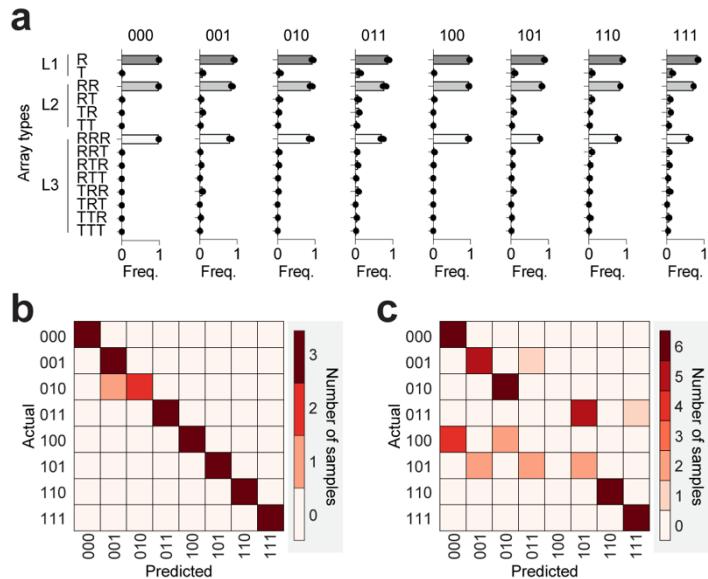
This PDF file includes:

Supplementary Figures 1 to 6

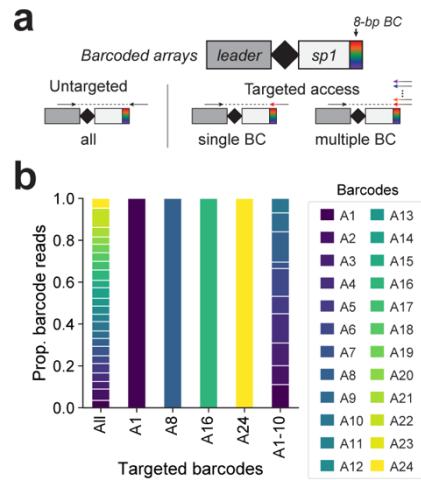
Supplementary Tables 1 to 3



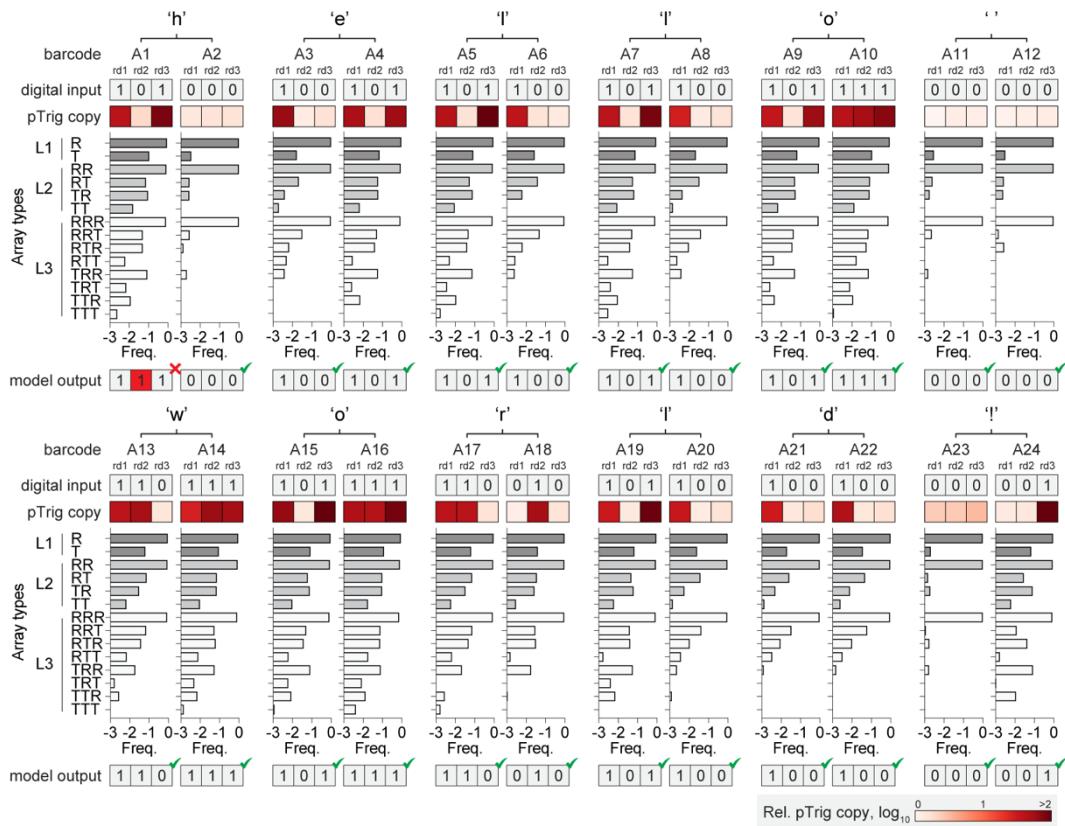
Supplementary Figure 1. Mapping spacers to their source location. (a) Proportion of source of newly incorporated spacers without (off, 0.0 V) and with (on, 0.5 V) electrical signal for 14 hours. (b) Genome-derived, (c) pRec-derived, and (d) pTrig-derived spacers were mapped to their protospacer location. Coverage was summed across 100 kb bins for genome or 100 bp bins for plasmids, and plotted. The three biological replicates without electrical stimulation (off, 0.0 V) are displayed in grey lines, and the three biological replicates with electrical stimulation (on, 0.5 V) are displayed in red lines. Genomic coordinate 0 is indexed as the midpoint of the *oriC* sequence. Spacers from the *soxR* gene region in pRec is excluded in the analysis as the region is present also in the genome. All measurements are based on three biological replicates. The number of spacers used in the analysis is displayed for each biological replicate.



Supplementary Figure 2. Classification using Euclidean distance between observed and reference datasets. For comparison, Euclidean distance between observed (new dataset) and reference array-type frequencies was calculated, and the 3-bit profile with minimum distance to the observed data was selected as the predicted 3-bit profile as previously described in Sheth et al., *Science* **358**, 1457-1461 (2017). **(a)** The reference array-type frequencies (derived from the first three independent experiments described in **Figure 2d**, averaged) used for the classification. The frequencies values are same as in **Figure 2d** but plotted in linear scale. **(b)** Classification of the training datasets (the first three independent datasets that we extracted reference array-type frequencies). For the classification of each sample, average 163,541 of total sequencing reads with 67,620 of expanded arrays (or 23,827 of L2/L3 arrays) with uniquely mapping spacers were used. Bead-based size enrichment was performed to enrich for expanded arrays and deplete unexpanded arrays. **(c)** Classification of the test datasets (6 additional independent datasets). For classification of each sample, an average of 172,788 total sequencing reads with 89,928 reads of expanded arrays (or 38,295 of L2/L3 arrays) that uniquely map spacers were used. Bead-based size enrichment was performed to enrich for expanded arrays and deplete unexpanded arrays.

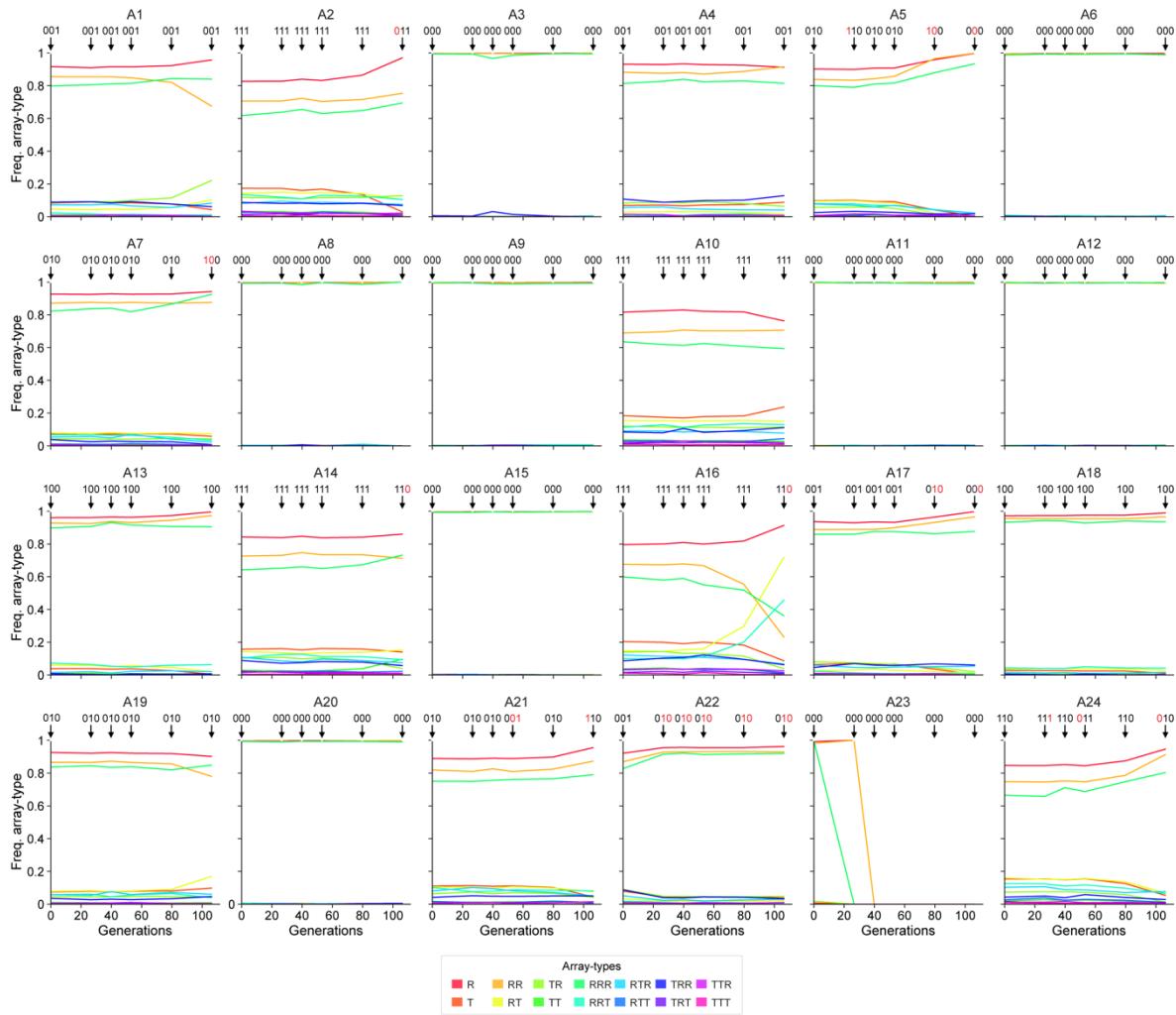


Supplementary Figure 3. Targeted access to specific barcoded cell populations in a mixed pool. (a) Schematic diagram of targeted amplification of barcoded CRISPR arrays in a mixed pool. (b) Targeted access to single or multiple barcoded cell populations in a mixed pool of 24 barcoded cell populations. For the targeted access to multiple (A1-10) barcoded cell populations, a single PCR reaction was performed using multiple primers simultaneously. All measurements are based on a single biological replicate.

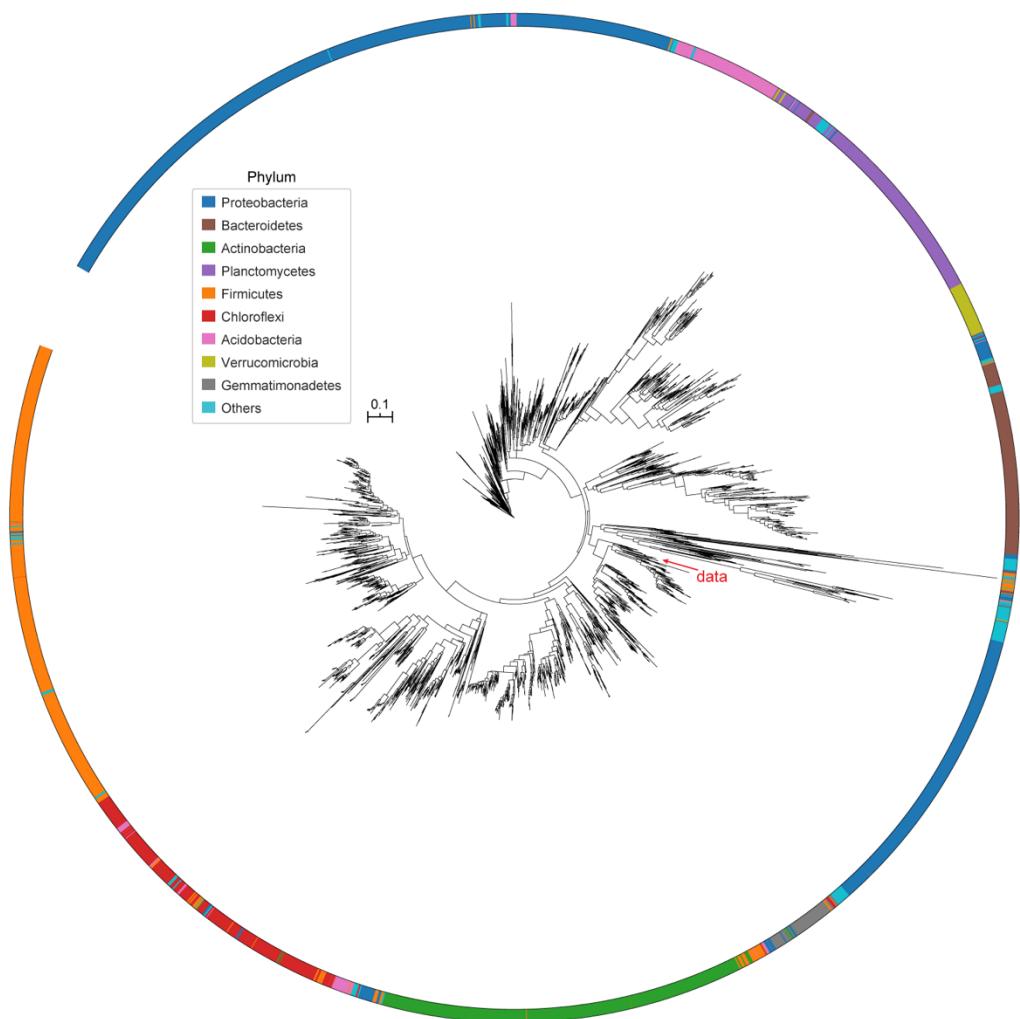


Supplementary Figure 4. ‘hello world!’ encoded in barcoded *E. coli* populations by DEC

6-bit encoding. DEC 6-bit encoding table is expected to have higher error rates for data reconstruction as described in **Extended Data Fig. 7**. When the same ‘hello world!’ text message was encoded using DEC 6-bit encoding table, 1 bit out of 72 bits for the text message was misclassified, resulting ‘xello world!’ returned from the classifier instead of ‘hello world!’. For classification of each barcoded cell population, an average of 247,906 total sequencing reads with 147,073 reads of expanded arrays (or 102,475 of L2/L3 arrays) that uniquely map spacers were used. Bead-based size enrichment was performed to enrich for expanded arrays and deplete unexpanded arrays. Frequencies of array-types are in \log_{10} scale. All measurements are based on a single experimental study.



Supplementary Figure 5. Array-type fluctuations over time in replicating cells. The array-type frequencies for each array lengths in each barcoded cell population over the course of the passage experiment in **Extended Data Fig. 10** are plotted. Samples were collected at the time points indicated by arrows (day 0, 4, 6, 8, 12, and 16). For each sampling time point, the measured array-type frequencies were used for data retrieval and the classification results are displayed (black: correct, red: wrong). For classification of each sample, an average of 82,860 total sequencing reads with 40,502 reads of expanded arrays (or 17,139 of L2/L3 arrays) that uniquely map spacers were used. Bead-based size enrichment was performed to enrich for expanded arrays and deplete unexpanded arrays. All measurements are based on three biological replicates.



Supplementary Figure 6. Phylogenetic diversity of a mixed microbial community of data-encoded *E. coli* cells and natural soil microbiota. Maximum-likelihood phylogenetic tree of all 4083 OTUs detected in the mixed community based on multiple sequence alignment of V4 region of 16S rRNA sequences using MAFFT (distance scale of 0.1).

Supplementary Table 1. Barcodes for CRISPR arrays

Array#	Array_sequence	BC
A1	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTAAGCGA TCAATCTAGCGCGACGTC	TAAG GC GA
A2	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTCACTAC TCAATCTAGCGCGACGTC	CGTA CTAG
A3	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGAGGAGAA TCAATCTAGCGCGACGTC	AGGC AGAA
A4	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTCCCTGAGC TCAATCTAGCGCGACGTC	TCCT GAGC
A5	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGGACTCT TCAATCTAGCGCGACGTC	GGAC TCCT
A6	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTAGGCATG TCAATCTAGCGCGACGTC	TAGG CATG
A7	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCTCT TCAATCTAGCGCGACGTC	CTCT CTAC
A8	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCGAGGCTG TCAATCTAGCGCGACGTC	CGAG GCTG
A9	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGAAAGGGCA TCAATCTAGCGCGACGTC	AAGA GCCA
A10	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTAGAGGA TCAATCTAGCGCGACGTC	GTAG AGGA
A11	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCTCATG TCAATCTAGCGCGACGTC	GCTC ATGA
A12	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGATCAGG TCAATCTAGCGCGACGTC	ATCT CAGG
A13	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGACTCG TCAATCTAGCGCGACGTC	ACTC GCTA
A14	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGGAGCT TCAATCTAGCGCGACGTC	GGAG CTAC
A15	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCGTAG TCAATCTAGCGCGACGTC	GC GT AGTA
A16	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCGGAGCT TCAATCTAGCGCGACGTC	CGGA GCCT
A17	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTACCGCT TCAATCTAGCGCGACGTC	TACG CTGC
A18	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGATCGCAG TCAATCTAGCGCGACGTC	ATGC GCAG
A19	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTAGGCT TCAATCTAGCGCGACGTC	TAGC GCTC
A20	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGACTGAGCG TCAATCTAGCGCGACGTC	ACTG AGCG
A21	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCTAACAG TCAATCTAGCGCGACGTC	CCTA AGAC
A22	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGCGATCAGG TCAATCTAGCGCGACGTC	CGAT CAGT
A23	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTGCACT TCAATCTAGCGCGACGTC	TGCA GCTA
A24	TGTTGTTGTGATACTATAAAGTTGGTAGATTGACTGGCTAAAAATCATTAATAATAAGTTATGTTAGA GTGTTCCCCG CGCCAGGGGATAAACCGAGCACAAATATCGCTCAACCCTACGGTCGACGT TCAATCTAGCGCGACGTC	TCGA CGTC

Colors: Leader-DR-Spacer1-BC-Pad

Supplementary Table 2. Simple parity check error correction

Actual input: 00000[0] / Error corrected output: 00000[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the 1 st 5 bits	Checksum	Checksum correct?	Can be recovered properly?
000	00[0]	100%	0	0	T	T

Actual input: 00001[1] / Error corrected output: 00001[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Checksum	Checksum correct?	Can be recovered properly?
000	01[1]	83.33%	1	1	T	T
000	00[1]	16.67%	0	0	F	T

Actual input: 00010[1] / Error corrected output: 00010[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Checksum	Checksum correct?	Can be recovered properly?
000	10[1]	83.33%	1	1	T	T
000	11[1]	16.67%	2	0	F	T

Actual input: 00011[0] / Error corrected output: 00011[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
000	11[0]	83.33%	2	0	T	T
000	01[0]	16.67%	1	1	F	T

Actual input: 00100[1] / Error corrected output: 00100[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
001	00[1]	100%	1	1	T	T

Actual input: 00101[0] / Error corrected output: 00101[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
001	01[0]	100%	2	0	T	T

Actual input: 00110[0] / Error corrected output: 00110[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
001	10[0]	100%	2	0	T	T

Actual input: 00111[1] / Error corrected output: 00111[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
001	11[1]	100%	3	1	T	T

Actual input: 01000[1] / Error corrected output: 01000[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
010	00[1]	100%	1	1	T	T

Actual input: 01001[0] / Error corrected output: 01001[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
010	01[0]	100%	2	0	T	T

Actual input: 01010[0] / Error corrected output: 01010[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
010	10[0]	100%	2	0	T	T

Actual input: 01011[1] / Error corrected output: 01011[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
010	11[1]	100%	3	1	T	T

Actual input: 01100[0] / Error corrected output: 01100[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
011	00[0]	83.33%	2	0	T	T
001	00[0]	16.67%	1	1	F	T

Actual input: 01101[1] / Error corrected output: 01101[1] (97.22%), 00100[1] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
011	01[1]	69.44%	3	1	T	T
011	00[1]	13.89%	2	0	F	T
001	01[1]	13.89%	2	0	F	T
001	00[1]	2.78%	1	1	T	F

Actual input: 01110[1] / Error corrected output: 01110[1] (97.22%), 00111[1] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
011	10[1]	69.44%	3	1	T	T
011	11[1]	13.89%	4	0	F	T
001	10[1]	13.89%	2	0	F	T
001	11[1]	2.78%	3	1	T	F

Actual input: 01111[0] / Error corrected output: 01111[0] (97.22%), 00101[0] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
011	11[0]	69.44%	4	0	T	T
011	01[0]	13.89%	3	1	F	T
001	11[0]	13.89%	3	1	F	T
001	01[0]	2.78%	2	0	T	F

Actual input: 10000[1] / Error corrected output: 10000[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
100	00[1]	100%	1	1	T	T

Actual input: 10001[0] / Error corrected output: 10001[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
100	01[0]	100%	2	0	T	T

Actual input: 10010[0] / Error corrected output: 10010[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
100	10[0]	100%	2	0	T	T

Actual input: 10011[1] / Error corrected output: 10011[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
100	11[1]	100%	3	1	T	T

Actual input: 10100[0] / Error corrected output: 10100[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
101	00[0]	83.33%	2	0	T	T
111	00[0]	16.67%	3	1	F	T

Actual input: 10101[1] / Error corrected output: 10101[1] (97.22%), 11100[1] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
101	01[1]	69.44%	3	1	T	T
101	00[1]	13.89%	2	0	F	T
111	01[1]	13.89%	4	0	F	T
111	00[1]	2.78%	3	1	T	F

Actual input: 10110[1] / Error corrected output: 10110[1] (97.22%), 11111[1] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
101	10[1]	69.44%	3	1	T	T
101	11[1]	13.89%	4	0	F	T
111	10[1]	13.89%	4	0	F	T
111	11[1]	2.78%	5	1	T	F

Actual input: 10111[0] / Error corrected output: 10111[0] (97.22%), 11101[0] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
101	11[0]	69.44%	4	0	T	T
101	01[0]	13.89%	3	1	F	T
111	11[0]	13.89%	5	1	F	T
111	01[0]	2.78%	4	0	T	F

Actual input: 11000[0] / Error corrected output: 11000[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
110	00[0]	83.33%	2	0	T	T
010	00[0]	16.67%	1	1	F	T

Actual input: 11001[1] / Error corrected output: 11001[1] (97.22%), 01000[1] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
110	01[1]	69.44%	3	1	T	T
110	00[1]	13.89%	2	0	F	T
010	01[1]	13.89%	2	0	F	T
010	00[1]	2.78%	1	1	T	F

Actual input: 11010[1] / Error corrected output: 11010[1] (97.22%), 01011[1] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
110	10[1]	69.44%	3	1	T	T
110	11[1]	13.89%	4	0	F	T
010	10[1]	13.89%	2	0	F	T
010	11[1]	2.78%	3	1	T	F

Actual input: 11011[0] / Error corrected output: 11011[0] (97.22%), 01001[0] (2.78%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
110	11[0]	69.44%	4	0	T	T
110	01[0]	13.89%	3	1	F	T
010	11[0]	13.89%	3	1	F	T
010	01[0]	2.78%	2	0	T	F

Actual input: 11100[1] / Error corrected output: 11100[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
111	00[1]	100%	3	1	T	T

Actual input: 11101[0] / Error corrected output: 11101[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
111	01[0]	100%	4	0	T	T

Actual input: 11110[0] / Error corrected output: 11110[0] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
111	10[0]	100%	4	0	T	T

Actual input: 11111[1] / Error corrected output: 11111[1] (100%)

Possible 1 st 3-bit call	Possible 2 nd 3-bit call	Prediction probability	# of 1 in the first 5 bits	Expected checksum	Checksum correct?	Can be recovered properly?
111	11[1]	100%	5	1	T	T

Supplementary Table 3. Primers used in this study

Seq_primer	Sequence
CB501	AATGATACGGCGACCACCGAGATCTACACTAGATCGCctggctaaaaaatcattaatta ataataggttatgtttaga
CB502	AATGATACGGCGACCACCGAGATCTACACCTCTCTATctggctaaaaaatcattaatta ataataggttatgtttaga
CB503	AATGATACGGCGACCACCGAGATCTACACTATCCTCTctggctaaaaaatcattaatta ataataggttatgtttaga
CB504	AATGATACGGCGACCACCGAGATCTACACAGAGTAGActggctaaaaaatcattaatta ataataggttatgtttaga
CB505	AATGATACGGCGACCACCGAGATCTACACGTAAGGAGctggctaaaaaatcattaatt aataataggttatgtttaga
CB506	AATGATACGGCGACCACCGAGATCTACACACTGCATAActggctaaaaaatcattaatta ataataggttatgtttaga
CB507	AATGATACGGCGACCACCGAGATCTACACAAGGAGTActggctaaaaaatcattaatta ataataggttatgtttaga
CB508	AATGATACGGCGACCACCGAGATCTACACCTAACGCCTctggctaaaaaatcattaatta ataataggttatgtttaga
CB509	AATGATACGGCGACCACCGAGATCTACACCGTCTAAActggctaaaaaatcattaatta ataataggttatgtttaga
CB510	AATGATACGGCGACCACCGAGATCTACACTCTCTCCGctggctaaaaaatcattaatta ataataggttatgtttaga
CB511	AATGATACGGCGACCACCGAGATCTACACTCGACTAGctggctaaaaaatcattaatta ataataggttatgtttaga
CB512	AATGATACGGCGACCACCGAGATCTACACTTCTAGCTctggctaaaaaatcattaatta ataataggttatgtttaga
CB513	AATGATACGGCGACCACCGAGATCTACACCTAGAGTctggctaaaaaatcattaatta ataataggttatgtttaga
CB514	AATGATACGGCGACCACCGAGATCTACACGCGTAAGActggctaaaaaatcattaatt aataataggttatgtttaga
CB515	AATGATACGGCGACCACCGAGATCTACACCTATTAAAGctggctaaaaaatcattaatta ataataggttatgtttaga
CB516	AATGATACGGCGACCACCGAGATCTACACAAGGCTATctggctaaaaaatcattaatta ataataggttatgtttaga
CB701	CAAGCAGAAGACGGCATACGAGATTCGCCTTAggttgagcgatgatatttgct
CB702	CAAGCAGAAGACGGCATACGAGATCTAGTACCGggttgagcgatgatatttgct
CB703	CAAGCAGAAGACGGCATACGAGATTCTGCCTggttgagcgatgatatttgct
CB704	CAAGCAGAAGACGGCATACGAGATGCTCAGGAgttgagcgatgatatttgct
CB705	CAAGCAGAAGACGGCATACGAGATAGGAGTCCggttgagcgatgatatttgct

CB706	CAAGCAGAAGACGGCATACGAGAT	CATGCCTAggtttagcgatataatgtct
CB707	CAAGCAGAAGACGGCATACGAGAT	GTTAGAGAGggtttagcgatataatgtct
CB708	CAAGCAGAAGACGGCATACGAGAT	CCTCTCTGggtttagcgatataatgtct
CB709	CAAGCAGAAGACGGCATACGAGAT	AGCGTAGCggtttagcgatataatgtct
CB710	CAAGCAGAAGACGGCATACGAGAT	CAGCCTCGggtttagcgatataatgtct
CB711	CAAGCAGAAGACGGCATACGAGAT	TGCCTCTTggtttagcgatataatgtct
CB712	CAAGCAGAAGACGGCATACGAGAT	TCCTCTACggtttagcgatataatgtct
CB713	CAAGCAGAAGACGGCATACGAGAT	TCATGAGCggtttagcgatataatgtct
CB714	CAAGCAGAAGACGGCATACGAGAT	CCTGAGATggtttagcgatataatgtct
CB715	CAAGCAGAAGACGGCATACGAGAT	TAGCGAGTggtttagcgatataatgtct
CB716	CAAGCAGAAGACGGCATACGAGAT	GTAGCTCCggtttagcgatataatgtct
CB717	CAAGCAGAAGACGGCATACGAGAT	TACTACGCggtttagcgatataatgtct
CB718	CAAGCAGAAGACGGCATACGAGAT	AGGCTCCGggtttagcgatataatgtct
CB719	CAAGCAGAAGACGGCATACGAGAT	GCAGCGTAggtttagcgatataatgtct
CB720	CAAGCAGAAGACGGCATACGAGAT	CTGCGCATggtttagcgatataatgtct
CB721	CAAGCAGAAGACGGCATACGAGAT	GAGCGCTAggtttagcgatataatgtct
CB722	CAAGCAGAAGACGGCATACGAGAT	CGCTCAGTggtttagcgatataatgtct
CB723	CAAGCAGAAGACGGCATACGAGAT	GTCTTAGGggtttagcgatataatgtct
CB724	CAAGCAGAAGACGGCATACGAGAT	ACTGATCGggtttagcgatataatgtct
CBR1	CTGGCTAAAAAAATCATTAATTATAATAGGTTATGTTAGAGTGTCCCCGC GCCAG	
CBI1	CGGGGATAAACCGAGCACAAATATCGCTCAAACC	

CB5XX: Illumina P5 adaptor sequence-BC (8 bp)-primer binding site

CB7XX: Illumina P7 adaptor sequence-BC (8 bp)-primer binding site

CBR1: Custom read1 sequencing primer (spiked into well 12)

CBI1: Custom index1 sequencing primer (spiked into well 13)

Barcoded array Sequence

seq primer

BC_Array_CB7	CAAGCAGAAGACGGCATACGAGAT	GACGTCGCGCTAGATTAGA
BC_Array_CBI	AACCGAGCACAAATATCGCTCAAACC	ACTACGG

BC_Array_CB7: Illumina P7 adaptor sequence-primer binding site

BC_Array_CBI: Custom index1 sequencing primer (spiked into well 13)

Random access Sequence

seq primer

RA701	CAAGCAGAAGACGGCATACGAGAT	CGCTAGATTAGATCGCCTTA
RA702	CAAGCAGAAGACGGCATACGAGAT	CGCTAGATTAGACTAGTACG
RA703	CAAGCAGAAGACGGCATACGAGAT	CGCTAGATTAGATTCTGCCT

RA704	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGCTAGGA
RA705	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAAGGAGTCC
RA706	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGACATGCCTA
RA707	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGTAGAGAG
RA708	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGACAGCCTCG
RA709	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGATGCCTCTT
RA710	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGATCCTCTAC
RA711	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGATCATGAGC
RA712	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGACCTGAGAT
RA713	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGATAGCGAGT
RA714	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGTAGCTCC
RA715	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGATACTACGC
RA716	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAAGGCTCCG
RA717	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGCAGCGTA
RA718	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGACTGCCAT
RA719	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGAGCGCTA
RA720	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGACGCTCAGT
RA721	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGTCTTAGG
RA722	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAACTGATCG
RA723	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGATAGCTGCA
RA724	CAAGCAGAAGACGGCATACGAGATCGCTAGATTAGAGACGTCGA

qPCR_primer	Sequence
genome-F	GCGAGCGATCCAGAAGATCT
genome-R	GGGTAAAGGATGCCACAGACA
pTrig-F	CGCTCTATGATCCAGTCGATT
pTrig-R	TCCGTATGCCATGCGTTAT